

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Dalla-Favera, Riccardo  
Chaganti, Raju S.K.
- (ii) TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS  
bcl-6
- (iii) NUMBER OF SEQUENCES: 9
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Cooper & Dunham LLP
  - (B) STREET: 1185 Avenue of the Americas
  - (C) CITY: New York
  - (D) STATE: New York
  - (E) COUNTRY: United States of America
  - (F) ZIP: 10036
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: White, John P.
  - (B) REGISTRATION NUMBER: 28,678
  - (C) REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US-Y
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (212) 278-0400
  - (B) TELEFAX: (212) 391-0525
  - (C) TELEX: 422523 COOP UI

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3720 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 328..2445

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCCCCCTCGA GCCTCGAACC GGAACCTCCA AATCCGAGAC GCTCTGCTTA TGAGGACCTC	60
GAAATATGCC GGCCAGTGAA AAAATCTTAT GGCTTTGAGG GCTTTTGTTT GGCCAGGGGC	120

AGTAAAAATC	TCGGAGAGCT	GACACCAAGT	CCTCCCCTGC	CACGTAGCAG	TGGTAAAGTC	180
CGAAGCTCAA	ATTCCGAGAA	TTGAGCTCTG	TTGATTCTTA	GAAGTGGGGT	TCTTAGAAGT	240
GGTGATGCAA	GAAGTTTCTA	GGAAAGGCCG	GACACCAGGT	TTTGAGCAAA	ATTTTGGACT	300
GTGAAGCAAG	GCATTGGTGA	AGACAAA	ATG GCC TCG CCG GCT GAC AGC TGT			351
			Met Ala Ser Pro Ala Asp Ser Cys			
			1	5		
ATC CAG TTC ACC CGC CAT GCC AGG GAT GTT CTT CTC AAC CTT AAT CGT						399
Ile Gln Phe Thr Arg His Ala Arg Asp Val Leu Asn Leu Asn Arg						
10		15		20		
CTC CGG AGT CGA GAC ATC TTG ACT GAT GTT GTC ATT GTT GTG AGC CGT						447
Leu Arg Ser Arg Asp Ile Leu Thr Asp Val Val Ile Val Val Ser Arg						
25		30		35		40
GAG CAG TTT AGA GCC CAT AAA ACG GTC CTC ATG GCC TGG AGA GGC CTG						495
Glu Gln Phe Arg Ala His Lys Thr Val Leu Met Ala Trp Arg Gly Leu						
		45		50		55
TTC TAT AGC ATC TTT ACA GAC CAG TTG AAA TGC AAC CTT AGT GTG ATC						543
Phe Tyr Ser Ile Phe Thr Asp Gln Leu Lys Cys Asn Leu Ser Val Ile						
		60		65		70
AAT CTA GAT CCT GAG ATC AAC CCT GAG GGA TTC TGC ATC CTC CTG GAC						591
Asn Leu Asp Pro Glu Ile Asn Pro Glu Gly Phe Cys Ile Leu Leu Asp						
		75		80		85
TTC ATG TAC ACA TCT CGG CTC AAT TTG CGG GAG GGC AAC ATC ATG GCT						639
Phe Met Tyr Thr Ser Arg Leu Asn Leu Arg Glu Gly Asn Ile Met Ala						
		90		95		100
GTG ATG GCC ACG GCT ATG TAC CTG CAG ATG GAG CAT GTT GTG GAC ACT						687
Val Met Ala Thr Ala Met Tyr Leu Gln Met Glu His Val Val Asp Thr						
105			110		115	120
TGC CGG AAG TTT ATT AAG GCC AGT GAA GCA GAG ATG GTT TCT GCC ATC						735
Cys Arg Lys Phe Ile Lys Ala Ser Glu Ala Glu Met Val Ser Ala Ile						
		125		130		135
AAG CCT CCT CGT GAA GAG TTC CTC AAC AGC CGG ATG CTG ATG CCC CAA						783
Lys Pro Pro Arg Glu Glu Phe Leu Asn Ser Arg Met Leu Met Pro Gln						
		140		145		150
GAC ATC ATG GCC TAT CGG GGT CGT GAG GTG GTG GAG AAC AAC CTG CCA						831
Asp Ile Met Ala Tyr Arg Gly Arg Glu Val Val Glu Asn Asn Leu Pro						
		155		160		165
CTG AGG AGC GCC CCT GGG TGT GAG AGC AGA GCC TTT GCC CCC AGC CTG						879
Leu Arg Ser Ala Pro Gly Cys Glu Ser Arg Ala Phe Ala Pro Ser Leu						
		170		175		180
TAC AGT GGC CTG TCC ACA CCG CCA GCC TCT TAT TCC ATG TAC AGC CAC						927
Tyr Ser Gly Leu Ser Thr Pro Pro Ala Ser Tyr Ser Met Tyr Ser His						
185			190		195	200
CTC CCT GTC AGC AGC CTC CTC TTC TCC GAT GAG GAG TTT CGG GAT GTC						975
Leu Pro Val Ser Ser Leu Leu Phe Ser Asp Glu Glu Phe Arg Asp Val						
		205		210		215

CGG	ATG	CCT	GTG	GCC	AAC	CCC	TTC	CCC	AAG	GAG	CGG	GCA	CTC	CCA	TGT	1023
Arg	Met	Pro	Val	Ala	Asn	Pro	Phe	Pro	Lys	Glu	Arg	Ala	Leu	Pro	Cys	
			220					225					230			
GAT	AGT	GCC	AGG	CCA	GTC	CCT	GGT	GAG	TAC	AGC	CGG	CCG	ACT	TTG	GAG	1071
Asp	Ser	Ala	Arg	Pro	Val	Pro	Gly	Glu	Tyr	Ser	Arg	Pro	Thr	Leu	Glu	
		235					240					245				
GTG	TCC	CCC	AAT	GTG	TGC	CAC	AGC	AAT	ATC	TAT	TCA	CCC	AAG	GAA	ACA	1119
Val	Ser	Pro	Asn	Val	Cys	His	Ser	Asn	Ile	Tyr	Ser	Pro	Lys	Glu	Thr	
	250					255					260					
ATC	CCA	GAA	GAG	GCA	CGA	AGT	GAT	ATG	CAC	TAC	AGT	GTG	GCT	GAG	GGC	1167
Ile	Pro	Glu	Glu	Ala	Arg	Ser	Asp	Met	His	Tyr	Ser	Val	Ala	Glu	Gly	
265					270					275					280	
CTC	AAA	CCT	GCT	GCC	CCC	TCA	GCC	CGA	AAT	GCC	CCC	TAC	TTC	CCT	TGT	1215
Leu	Lys	Pro	Ala	Ala	Pro	Ser	Ala	Arg	Asn	Ala	Pro	Tyr	Phe	Pro	Cys	
				285					290					295		
GAC	AAG	GCC	AGC	AAA	GAA	GAA	GAG	AGA	CCC	TCC	TCG	GAA	GAT	GAG	ATT	1263
Asp	Lys	Ala	Ser	Lys	Glu	Glu	Glu	Arg	Pro	Ser	Ser	Glu	Asp	Glu	Ile	
			300					305					310			
GCC	CTG	CAT	TTC	GAG	CCC	CCC	AAT	GCA	CCC	CTG	AAC	CGG	AAG	GGT	CTG	1311
Ala	Leu	His	Phe	Glu	Pro	Pro	Asn	Ala	Pro	Leu	Asn	Arg	Lys	Gly	Leu	
		315					320					325				
GTT	AGT	CCA	CAG	AGC	CCC	CAG	AAA	TCT	GAC	TGC	CAG	CCC	AAC	TCG	CCC	1359
Val	Ser	Pro	Gln	Ser	Pro	Gln	Lys	Ser	Asp	Cys	Gln	Pro	Asn	Ser	Pro	
	330					335					340					
ACA	GAG	GCC	TGC	AGC	AGT	AAG	AAT	GCC	TGC	ATC	CTC	CAG	GGT	TCT	GGC	1407
Thr	Glu	Ala	Cys	Ser	Ser	Lys	Asn	Ala	Cys	Ile	Leu	Gln	Gly	Ser	Gly	
345					350					355					360	
TCC	CCT	CCA	GCC	AAG	AGC	CCC	ACT	GAC	CCC	AAA	GCC	TGC	AGC	TGG	AAG	1455
Ser	Pro	Pro	Ala	Lys	Ser	Pro	Thr	Asp	Pro	Lys	Ala	Cys	Ser	Trp	Lys	
				365					370					375		
AAA	TAC	AAG	TTC	ATC	GTG	CTC	AAC	AGC	CTC	AAC	CAG	AAT	GCC	AAA	CCA	1503
Lys	Tyr	Lys	Phe	Ile	Val	Leu	Asn	Ser	Leu	Asn	Gln	Asn	Ala	Lys	Pro	
			380					385					390			
GGG	GGG	CCT	GAG	CAG	GCT	GAG	CTG	GGC	CGC	CTT	TCC	CCA	CGA	GCC	TAC	1551
Gly	Gly	Pro	Glu	Gln	Ala	Glu	Leu	Gly	Arg	Leu	Ser	Pro	Arg	Ala	Tyr	
		395				400						405				
ACG	GCC	CCA	CCT	GCC	TGC	CAG	CCA	CCC	ATG	GAG	CCT	GAG	AAC	CTT	GAC	1599
Thr	Ala	Pro	Pro	Ala	Cys	Gln	Pro	Pro	Met	Glu	Pro	Glu	Asn	Leu	Asp	
	410					415					420					
CTC	CAG	TCC	CCA	ACC	AAG	CTG	AGT	GCC	AGC	GGG	GAG	GAC	TCC	ACC	ATC	1647
Leu	Gln	Ser	Pro	Thr	Lys	Leu	Ser	Ala	Ser	Gly	Glu	Asp	Ser	Thr	Ile	
425					430					435					440	
CCA	CAA	GCC	AGC	CGG	CTC	AAT	AAC	ATC	GTT	AAC	AGG	TCC	ATG	ACG	GGC	1695
Pro	Gln	Ala	Ser	Arg	Leu	Asn	Asn	Ile	Val	Asn	Arg	Ser	Met	Thr	Gly	
				445					450					455		
TCT	CCC	CGC	AGC	AGC	AGC	GAG	AGC	CAC	TCA	CCA	CTC	TAC	ATG	CAC	CCC	1743
Ser	Pro	Arg	Ser	Ser	Ser	Glu	Ser	His	Ser	Pro	Leu	Tyr	Met	His	Pro	

460				465				470								
CCG Pro	AAG Lys	TGC Cys 475	ACG Thr	TCC Ser	TGC Cys	GGC Gly	TCT Ser 480	CAG Gln	TCC Ser	CCA Pro	CAG Gln	CAT His 485	GCA Ala	GAG Glu	ATG Met	1791
TGC Cys 490	CTC Leu	CAC His	ACC Thr	GCT Ala	GGC Gly	CCC Pro 495	ACG Thr	TTC Phe	GCT Ala	GAG Glu	GAG Glu 500	ATG Met	GGA Gly	GAG Glu	ACC Thr	1839
CAG Gln 505	TCT Ser	GAG Glu	TAC Tyr	TCA Ser	GAT Asp 510	TCT Ser	AGC Ser	TGT Cys	GAG Glu	AAC Asn 515	GGG Gly	GCC Ala	TTC Phe	TTC Phe	TGC Cys 520	1887
AAT Asn	GAG Glu	TGT Cys	GAC Asp	TGC Cys 525	CGC Arg	TTC Phe	TCT Ser	GAG Glu	GAG Glu 530	GCC Ala	TCA Ser	CTC Leu	AAG Lys	AGG Arg 535	CAC His	1935
ACG Thr	CTG Leu	CAG Gln	ACC Thr 540	CAC His	AGT Ser	GAC Asp	AAA Lys	CCC Pro 545	TAC Tyr	AAG Lys	TGT Cys	GAC Asp	CGC Arg 550	TGC Cys	CAG Gln	1983
GCC Ala	TCC Ser	TTC Phe 555	CGC Arg	TAC Tyr	AAG Lys	GGC Gly	AAC Asn 560	CTC Leu	GCC Ala	AGC Ser	CAC His	AAG Lys 565	ACC Thr	GTC Val	CAT His	2031
ACC Thr	GGT Gly 570	GAG Glu	AAA Lys	CCC Pro	TAT Tyr	CGT Arg 575	TGC Cys	AAC Asn	ATC Ile	TGT Cys	GGG Gly 580	GCC Ala	CAG Gln	TTC Phe	AAC Asn	2079
CGG Arg 585	CCA Pro	GCC Ala	AAC Asn	CTG Leu	AAA Lys 590	ACC Thr	CAC His	ACT Thr	CGA Arg	ATT Ile 595	CAC His	TCT Ser	GGA Gly	GAG Glu	AAG Lys 600	2127
CCC Pro	TAC Tyr	AAA Lys	TGC Cys	GAA Glu 605	ACC Thr	TGC Cys	GGA Gly	GCC Ala	AGA Arg 610	TTT Phe	GTA Val	CAG Gln	GTG Val	GCC Ala 615	CAC His	2175
CTC Leu	CGT Arg	GCC Ala	CAT His 620	GTG Val	CTT Leu	ATC Ile	CAC His	ACT Thr 625	GGT Gly	GAG Glu	AAG Lys	CCC Pro	TAT Tyr 630	CCC Pro	TGT Cys	2223
GAA Glu	ATC Ile	TGT Cys 635	GGC Gly	ACC Thr	CGT Arg	TTC Phe	CGG Arg 640	CAC His	CTT Leu	CAG Gln	ACT Thr	CTG Leu 645	AAG Lys	AGC Ser	CAC His	2271
CTG Leu	CGA Arg 650	ATC Ile	CAC His	ACA Thr	GGA Gly	GAG Glu 655	AAA Lys	CCT Pro	TAC Tyr	CAT His	TGT Cys 660	GAG Glu	AAG Lys	TGT Cys	AAC Asn	2319
CTG Leu 665	CAT His	TTC Phe	CGT Arg	CAC His	AAA Lys 670	AGC Ser	CAG Gln	CTG Leu	CGA Arg	CTT Leu 675	CAC His	TTG Leu	CGC Arg	CAG Gln	AAG Lys 680	2367
CAT His	GGC Gly	GCC Ala	ATC Ile	ACC Thr 685	AAC Asn	ACC Thr	AAG Lys	GTG Val	CAA Gln 690	TAC Tyr	CGC Arg	GTG Val	TCA Ser	GCC Ala 695	ACT Thr	2415
GAC Asp	CTG Leu	CCT Pro	CCG Pro 700	GAG Glu	CTC Leu	CCC Pro	AAA Lys	GCC Ala 705	TGC Cys	TGAAGCATGG	AGTGTGATG					2465

CTTTCGTCTC CAGCCCCTTC TCAGAATCTA CCCAAAGGAT ACTGTAACAC TTTACAATGT	2525
TCATCCCATG ATGTAGTGCC TCTTTCATCC ACTAGTGCAA ATCATAGCTG GGGGTTGGGG	2585
GTGGTGGGGG TCGGGGCCTG GGGGACTGGG AGCCGCAGCA GCTCCCCCTC CCCCCTGACC	2645
ATAAAACATT AAGAAAATCA TATTGCTTCT TCTCCTATGT GNNNNNNNNNN NNNNNNNNNNN	2705
NNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN	2765
NNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN	2825
NNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN	2885
NNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN	2945
NNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN	3005
NNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN	3065
NNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN	3125
NNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN	3185
NNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN NNNNNNNNNNN	3245
NTTTAAGTAT TGCATCTGTA TAAGTAAGAA AATATTTTGT CTAAAATGCC TCAGTGTATT	3305
TGTATTTTTT TGCAAGTGGG GGGTTACAAT TTACCCAGTG TGTATTAAAA AAAACCCAAA	3365
GAACCCAAAA ATCTCCAGAA GGAAAAATGT GTAATTTTGT TCTAGTTTTT AGTTTGTATA	3425
TACCCGTACA ACGTGTCTTC ACGGTGCCTT TTTTCACGGA AGTTTTCAAT GATGGGCGAG	3485
CGTGCACCAT CCCTTTTTGA AGTGTAGGCA GACACAGGGA CTTGAAGTTG TTACTAACTA	3545
AACTCTCTTT GGGAAATGTTT GTCTCATCCC ANTCTGCGTC ATGCTTGTGT GATAACTACT	3605
CCGGAGACAG GGTTTGGCTG TGTCTAAACT GCATTACCGC GTTGTAAAAA ATAGCTGTAC	3665
CAATATAAGA ATAAAATGTT GGAAAGTCGC AAAAAAAAAA AAAAAAAAAA AAAAA	3720

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	Ser	Pro	Ala	Asp	Ser	Cys	Ile	Gln	Phe	Thr	Arg	His	Ala	Arg
1				5					10					15	
Asp	Val	Leu	Leu	Asn	Leu	Asn	Arg	Leu	Arg	Ser	Arg	Asp	Ile	Leu	Thr
		20					25						30		
Asp	Val	Val	Ile	Val	Val	Ser	Arg	Glu	Gln	Phe	Arg	Ala	His	Lys	Thr
		35					40						45		

Val	Leu	Met	Ala	Trp	Arg	Gly	Leu	Phe	Tyr	Ser	Ile	Phe	Thr	Asp	Gln
50						55					60				
Leu	Lys	Cys	Asn	Leu	Ser	Val	Ile	Asn	Leu	Asp	Pro	Glu	Ile	Asn	Pro
65					70					75					80
Glu	Gly	Phe	Cys	Ile	Leu	Leu	Asp	Phe	Met	Tyr	Thr	Ser	Arg	Leu	Asn
				85					90					95	
Leu	Arg	Glu	Gly	Asn	Ile	Met	Ala	Val	Met	Ala	Thr	Ala	Met	Tyr	Leu
			100					105					110		
Gln	Met	Glu	His	Val	Val	Asp	Thr	Cys	Arg	Lys	Phe	Ile	Lys	Ala	Ser
		115					120					125			
Glu	Ala	Glu	Met	Val	Ser	Ala	Ile	Lys	Pro	Pro	Arg	Glu	Glu	Phe	Leu
	130						135				140				
Asn	Ser	Arg	Met	Leu	Met	Pro	Gln	Asp	Ile	Met	Ala	Tyr	Arg	Gly	Arg
145					150					155					160
Glu	Val	Val	Glu	Asn	Asn	Leu	Pro	Leu	Arg	Ser	Ala	Pro	Gly	Cys	Glu
				165					170					175	
Ser	Arg	Ala	Phe	Ala	Pro	Ser	Leu	Tyr	Ser	Gly	Leu	Ser	Thr	Pro	Pro
			180					185					190		
Ala	Ser	Tyr	Ser	Met	Tyr	Ser	His	Leu	Pro	Val	Ser	Ser	Leu	Leu	Phe
		195					200					205			
Ser	Asp	Glu	Glu	Phe	Arg	Asp	Val	Arg	Met	Pro	Val	Ala	Asn	Pro	Phe
	210					215					220				
Pro	Lys	Glu	Arg	Ala	Leu	Pro	Cys	Asp	Ser	Ala	Arg	Pro	Val	Pro	Gly
225					230					235					240
Glu	Tyr	Ser	Arg	Pro	Thr	Leu	Glu	Val	Ser	Pro	Asn	Val	Cys	His	Ser
				245					250					255	
Asn	Ile	Tyr	Ser	Pro	Lys	Glu	Thr	Ile	Pro	Glu	Glu	Ala	Arg	Ser	Asp
			260					265					270		
Met	His	Tyr	Ser	Val	Ala	Glu	Gly	Leu	Lys	Pro	Ala	Ala	Pro	Ser	Ala
		275					280					285			
Arg	Asn	Ala	Pro	Tyr	Phe	Pro	Cys	Asp	Lys	Ala	Ser	Lys	Glu	Glu	Glu
	290					295					300				
Arg	Pro	Ser	Ser	Glu	Asp	Glu	Ile	Ala	Leu	His	Phe	Glu	Pro	Pro	Asn
305					310					315					320
Ala	Pro	Leu	Asn	Arg	Lys	Gly	Leu	Val	Ser	Pro	Gln	Ser	Pro	Gln	Lys
				325					330					335	
Ser	Asp	Cys	Gln	Pro	Asn	Ser	Pro	Thr	Glu	Ala	Cys	Ser	Ser	Lys	Asn
			340					345					350		
Ala	Cys	Ile	Leu	Gln	Gly	Ser	Gly	Ser	Pro	Pro	Ala	Lys	Ser	Pro	Thr
		355					360					365			
Asp	Pro	Lys	Ala	Cys	Ser	Trp	Lys	Lys	Tyr	Lys	Phe	Ile	Val	Leu	Asn

370										375										380									
Ser	Leu	Asn	Gln	Asn	Ala	Lys	Pro	Gly	Gly	Pro	Glu	Gln	Ala	Glu	Leu														
385					390					395					400														
Gly	Arg	Leu	Ser	Pro	Arg	Ala	Tyr	Thr	Ala	Pro	Pro	Ala	Cys	Gln	Pro														
				405					410					415															
Pro	Met	Glu	Pro	Glu	Asn	Leu	Asp	Leu	Gln	Ser	Pro	Thr	Lys	Leu	Ser														
			420					425					430																
Ala	Ser	Gly	Glu	Asp	Ser	Thr	Ile	Pro	Gln	Ala	Ser	Arg	Leu	Asn	Asn														
		435					440					445																	
Ile	Val	Asn	Arg	Ser	Met	Thr	Gly	Ser	Pro	Arg	Ser	Ser	Ser	Glu	Ser														
	450					455					460																		
His	Ser	Pro	Leu	Tyr	Met	His	Pro	Pro	Lys	Cys	Thr	Ser	Cys	Gly	Ser														
465					470					475					480														
Gln	Ser	Pro	Gln	His	Ala	Glu	Met	Cys	Leu	His	Thr	Ala	Gly	Pro	Thr														
				485					490					495															
Phe	Ala	Glu	Glu	Met	Gly	Glu	Thr	Gln	Ser	Glu	Tyr	Ser	Asp	Ser	Ser														
			500					505					510																
Cys	Glu	Asn	Gly	Ala	Phe	Phe	Cys	Asn	Glu	Cys	Asp	Cys	Arg	Phe	Ser														
		515					520				525																		
Glu	Glu	Ala	Ser	Leu	Lys	Arg	His	Thr	Leu	Gln	Thr	His	Ser	Asp	Lys														
	530					535					540																		
Pro	Tyr	Lys	Cys	Asp	Arg	Cys	Gln	Ala	Ser	Phe	Arg	Tyr	Lys	Gly	Asn														
545					550					555					560														
Leu	Ala	Ser	His	Lys	Thr	Val	His	Thr	Gly	Glu	Lys	Pro	Tyr	Arg	Cys														
				565					570					575															
Asn	Ile	Cys	Gly	Ala	Gln	Phe	Asn	Arg	Pro	Ala	Asn	Leu	Lys	Thr	His														
			580				585						590																
Thr	Arg	Ile	His	Ser	Gly	Glu	Lys	Pro	Tyr	Lys	Cys	Glu	Thr	Cys	Gly														
		595					600					605																	
Ala	Arg	Phe	Val	Gln	Val	Ala	His	Leu	Arg	Ala	His	Val	Leu	Ile	His														
	610					615					620																		
Thr	Gly	Glu	Lys	Pro	Tyr	Pro	Cys	Glu	Ile	Cys	Gly	Thr	Arg	Phe	Arg														
625					630					635					640														
His	Leu	Gln	Thr	Leu	Lys	Ser	His	Leu	Arg	Ile	His	Thr	Gly	Glu	Lys														
				645					650					655															
Pro	Tyr	His	Cys	Glu	Lys	Cys	Asn	Leu	His	Phe	Arg	His	Lys	Ser	Gln														
			660					665					670																
Leu	Arg	Leu	His	Leu	Arg	Gln	Lys	His	Gly	Ala	Ile	Thr	Asn	Thr	Lys														
		675					680					685																	
Val	Gln	Tyr	Arg	Val	Ser	Ala	Thr	Asp	Leu	Pro	Pro	Glu	Leu	Pro	Lys														
	690					695					700																		

Ala Cys  
705

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 103 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Asp	Gly	Ser	Phe	Val	Gln	His	Ser	Val	Arg	Val	Leu	Gln	Glu	Leu	Asn	
1				5					10					15		
Lys	Gln	Arg	Glu	Lys	Gly	Gln	Tyr	Cys	Asp	Ala	Thr	Leu	Asp	Val	Gly	
			20					25					30			
Gly	Leu	Val	Phe	Lys	Ala	His	Trp	Ser	Val	Leu	Ala	Cys	Cys	Ser	His	
			35				40					45				
Phe	Phe	Gln	Ser	Leu	Tyr	Gly	Asp	Gly	Ser	Gly	Gly	Ser	Val	Val	Leu	
	50					55					60					
Pro	Ala	Gly	Phe	Ala	Glu	Ile	Phe	Gly	Leu	Leu	Leu	Asp	Phe	Phe	Tyr	
65					70					75					80	
Thr	Gly	His	Leu	Ala	Leu	Thr	Ser	Gly	Asn	Arg	Asp	Gln	Val	Leu	Leu	
			85						90					95		
Ala	Ala	Arg	Glu	Leu	Arg	Val										
					100											

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 107 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Asp	Thr	Ala	Ser	His	Ser	Leu	Val	Leu	Leu	Gln	Gln	Leu	Asn	Met	
1					5				10					15		
Gln	Arg	Glu	Phe	Gly	Phe	Leu	Cys	Asp	Cys	Thr	Val	Ala	Ile	Gly	Asp	
			20					25						30		



Val Tyr Phe Lys Ala His Arg Ala Val Leu Ala Ala Phe Ser Asn Tyr  
35 40 45  
Phe Lys Met Ile Phe Ile His Gln Thr Ser Glu Cys Ile Lys Ile Gln  
50 55 60  
Pro Thr Asp Ile Gln Pro Asp Ile Phe Ser Tyr Leu Leu His Ile Met  
65 70 75 80  
Tyr Thr Gly Lys Gly Pro Lys Gln Ile Val Asp His Ser Arg Leu Glu  
85 90 95  
Glu Gly Ile Arg Phe Leu His Ala Asp Tyr Leu  
100 105

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 106 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Asn Asn Ser Ser Glu Leu Ile Ala Val Ile Asn Gly Phe Arg Asn  
1 5 10 15  
Ser Gly Arg Phe Cys Asp Ile Ser Ile Val Ile Asn Asp Glu Arg Ile  
20 25 30  
Asn Ala His Lys Leu Ile Leu Ser Gly Ala Ser Glu Tyr Phe Ser Ile  
35 40 45  
Leu Phe Ser Asn Asn Phe Ile Asp Ser Asn Glu Tyr Glu Val Asn Leu  
50 55 60  
Ser His Leu Asp Tyr Gln Ser Val Asn Asp Leu Ile Asp Tyr Ile Tyr  
65 70 75 80  
Gly Ile Pro Leu Ser Leu Thr Asn Asp Asn Val Lys Tyr Ile Leu Ser  
85 90 95  
Thr Ala Asp Phe Leu Gln Ile Gly Ser Ala  
100 105

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 108 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

Cys Leu Arg Trp Asn Asn His Gln Ser Asn Leu Leu Ser Val Phe Asp
1          5          10          15
Gln Leu Leu His Ala Glu Thr Phe Thr Asp Val Thr Leu Ala Val Glu
          20          25          30
Gly Gln His Leu Lys Ala His Lys Asn Val Leu Ser Ala Cys Ser Pro
          35          40          45
Tyr Phe Asn Thr Leu Phe Val Ser His Pro Glu Lys His Pro Ile Val
          50          55          60
Ile Leu Lys Asp Val Pro Tyr Ser Asp Met Lys Ser Leu Leu Asp Phe
65          70          75          80
Met Tyr Arg Gly Glu Val Ser Val Asp Gln Glu Arg Leu Thr Ala Phe
          85          90          95
Leu Arg Val Ala Glu Ser Leu Arg Ile Lys Gly Leu
          100          105

```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

Gln Tyr Ser Asn Glu Gln His Thr Ala Arg Ser Phe Asp Ala Met Asn
1          5          10          15
Glu Met Arg Lys Gln Lys Gln Leu Cys Asp Val Ile Leu Val Ala Asp
          20          25          30
Asp Val Glu Ile His Ala His Arg Met Val Leu Ala Ser Cys Ser Pro
          35          40          45
Tyr Phe Tyr Ala Met Phe Thr Ser Phe Glu Glu Ser Arg Gln Ala Arg
          50          55          60
Ile Thr Leu Gln Ser Val Asp Ala Arg Ala Leu Glu Leu Leu Ile Asp
65          70          75          80
Tyr Val Tyr Thr Ala Thr Val Glu Val Asn Glu Asp Asn Val Gln Val
          85          90          95
Leu Leu Thr Ala Ala Asn Leu Leu Gln Leu Thr Asp Val
          100          105

```

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 105 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gln	Leu	Gln	Asn	Pro	Ser	His	Pro	Thr	Gly	Leu	Leu	Cys	Lys	Ala	Asn	1	5	10	15
Gln	Met	Arg	Leu	Ala	Gly	Thr	Leu	Cys	Asp	Val	Val	Ile	Met	Val	Asp	20	25	30	
Ser	Gln	Glu	Phe	His	Ala	His	Arg	Thr	Val	Leu	Ala	Cys	Thr	Ser	Lys	35	40	45	
Met	Phe	Glu	Ile	Leu	Phe	His	Arg	Asn	Ser	Gln	His	Tyr	Thr	Leu	Asp	50	55	60	
Phe	Leu	Ser	Pro	Lys	Thr	Phe	Gln	Gln	Ile	Leu	Glu	Tyr	Ala	Tyr	Thr	65	70	75	80
Ala	Thr	Leu	Gln	Ala	Lys	Ala	Glu	Asp	Leu	Asp	Asp	Leu	Leu	Tyr	Ala	85	90	95	
Ala	Glu	Ile	Leu	Glu	Ile	Glu	Tyr	Leu								100	105		

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 110 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Cys	Leu	Gln	Phe	Thr	Arg	His	Ala	Ser	Asp	Val	Leu	Leu	Asn	Leu	Asn	1	5	10	15
Arg	Leu	Arg	Ser	Arg	Asp	Ile	Leu	Thr	Asp	Val	Val	Ile	Val	Val	Ser	20	25	30	
Arg	Glu	Gln	Phe	Arg	Ala	His	Lys	Thr	Val	Leu	Met	Ala	Cys	Ser	Gly	35	40	45	
Leu	Phe	Tyr	Ser	Ile	Phe	Thr	Asp	Gln	Leu	Lys	Cys	Asn	Leu	Ser	Val	50	55	60	

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Ile	Asn	Leu	Asp	Pro	Glu	Ile	Asn	Pro	Glu	Gly	Phe	Cys	Ile	Leu	Leu
65					70					75				80	
Asp	Phe	Met	Tyr	Thr	Ser	Arg	Leu	Asn	Leu	Arg	Glu	Gly	Asn	Ile	Met
				85					90					95	
Ala	Val	Met	Ala	Thr	Ala	Met	Tyr	Leu	Gln	Met	Glu	His	Val		
			100					105					110		